

SEQUENCE LISTING

<100> GENERAL INFORMATION:

<160> NUMBER OF SEQ ID NOS: 48

<200> SEQUENCE CHARACTERISTICS:

<210> SEQ ID NO 1

<211> LENGTH: 33

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence synthetic primer

<400> SEQUENCE: 1

cataaaattt ctaagacgaa ggtccctat gtc 33

<200> SEQUENCE CHARACTERISTICS:

<210> SEQ ID NO 2

<211> LENGTH: 33

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence synthetic primer

<400> SEQUENCE: 2

gagagaaagt tccccgtgtg aattctagct agg 33

<200> SEQUENCE CHARACTERISTICS:

<210> SEQ ID NO 3

<211> LENGTH: 2836

<212> TYPE: DNA

<213> ORGANISM: Ehrlichia risticii

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (175)..(2721)

<400> SEQUENCE: 3

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ttaaatttta tgatttltta taataaaat agatataaaa tttatagatt l.lataaattt 120
ttcataacaa aggactatcc tccttgcata aaatttctaa gacgaaaaat cccl atg 177
Met

tca	aat	gaa	aca	ctt	ttg	agc	gta	ctt	tct	gal	gaa	ucg	cac	ttt	gct	225
Ser	Asn	Glu	Thr	Leu	Leu	Ser	Val	Leu	Ser	Asp	Glu	Thr	His	Phe	Ala	
			5						10				15			
aat	cta	gtt	gat	gaa	ctt	ctt	ctc	atc	ttg	gll	aaa	gac	ugt	att	ttc	273
Asn	Leu	Val	Asp	Glu	Leu	Leu	Leu	Ile	Leu	Val	Lys	Asp	Ser	Ile	Phe	
			20				25				30					
act	caa	gta	atu	aaa	ggc	gag	gga	aag	aca	gaa	tta	aaa	gac	ata	ctt	321
Thr	Gln	Val	Ile	Lys	Gly	Glu	Gly	Lys	Thr	Glu	Leu	Lys	Asp	Ile	Leu	
			35			40				45						
aca	gac	aac	act	ggt	aag	ttt	aaa	gaa	ctt	ata	guu	ugt	gca	ggt	aaa	369
Thr	Asp	Asn	Thr	Gly	Lys	Phe	Lys	Glu	Leu	Ile	Glu	Ser	Ala	Gly	Lys	
			50		55				60					65		
gac	ata	cta	uuu	gug	ata	ctt	aca	gac	aat	acc	ggc	aat	ttt	aaa	gga	417
Asp	Ile	Leu	Lys	Glu	Ile	Leu	Thr	Asp	Asn	Thr	Gly	Asn	Phe	Lys	Gly	
			70				75						80			
ctt	ata	gaa	ggt	aat	ggt	aag	acq	qag	gca	aaa	gag	gta	cgc	act	aat	465
Leu	Ile	Glu	Gly	Asn	Gly	Lys	Thr	Glu	Ala	Lys	Glu	Val	Arg	Thr	Asn	

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      85      90      95
gaa aaa ttc aag gag ctt ttt gga agc aat ggt aag gac ata ctg aaa 513
Glu Lys Phe Lys Glu Leu Phe Gly Ser Asn Gly Lys Asp Ile Leu Lys
100
gac att ctt act gat aac acc ggt aac ttt aaa ggc cll ata gaa agt 561
Asp Ile Leu Thr Asp Asn Thr Gly Asn Phe Lys Gly Leu Ile Glu Ser
115
gca gct aag ggt aag ctg aaa gat ctt ctt att qat gaa aaa ttt caa 609
Ala Ala Lys Gly Lys Leu Lys Asp Leu Leu Ile Asp Glu Lys Phe Gln
130
aaa tta ttc gag gat gaa acg aaa gct ggt cgt gta aaa gaa ata ctt 657
Lys Leu Phe Glu Asp Glu Thr Lys Ala Gly Arg Val Lys Glu Ile Leu
150
aca gac agc aac gct aag gaa atu ctc aca aat gaa gta gca aaa gag 705
Thr Asp Ser Asn Ala Lys Glu Ile Leu Thr Asn Glu Val Ala Lys Glu
165
gla cta aau tcc gat aaa ttc aag gag gca ala act ggc gat ggt aag 753
Val Leu Lys Ser Asp Lys Phe Lys Glu Ala Ile Thr Gly Asp Gly Lys
180
gac gca cta aaa gag ata ctt act lgt gat uuu ttt aaa gag gct gta 801
Asp Ala Leu Lys Glu Ile Leu Thr Cys Asp Lys Phe Lys Glu Ala Val
195
acu ggc aet ggt aaa gac ata cta aaa ggt ata ctt aca gat agc act 849
Thr Gly Asn Gly Lys Asp Ile Leu Lys Gly Ile Leu Thr Asp Ser Thr
210
ggt aaa ttt aaa gaa ctt ala gaa agt uct agt aaa gac ata cta aaa 897
Gly Lys Phe Lys Glu Leu Ile Glu Ser Thr Ser Lys Asp Ile Leu Lys
230
gag ata ctt aca gat aat acc ggt aac ttt aaa ggc ctt ata gaa agc 945
Glu Ile Leu Thr Asp Asn Thr Gly Asn Phe Lys Gly Leu Ile Glu Ser
245
act ggc aag gag aaa gta aaa gaa ctt ctt atc gat ggg aag ttt aag 993
Thr Gly Lys Glu Lys Val Lys Glu Leu Leu Ile Asp Gly Lys Phe Lys
260
gac ctg ttt act gat gca aca aaa gcc ggt tal gta aaa gaa atu ctc1041
Asp Leu Phe Thr Asp Ala Thr Lys Ala Gly Tyr Val Lys Glu Ile Leu
275
acg aac gal aca gct aag gaa gta ctt aca gat caa aca gca aag gag1089
Thr Asn Asp Thr Ala Lys Glu Val Leu Thr Asp Gln Thr Ala Lys Glu
290
gtc cta aaa gat agt aca gct uuu qac ata tta aag gac aca aac gca1137
Val Leu Lys Asp Ser Thr Ala Lys Asp Ile Leu Lys Asp Thr Asn Ala
310
gct gcg gta cta aaa aac agc aca gct aaa gaa ata ctt aca aac caa1185
Ala Ala Val Leu Lys Asn Ser Thr Ala Lys Glu Ile Leu Thr Asn Gln
325
acc gct uuu gaa gtg ctt aca gat ggt aca tcc aaa gaa gta cta aaal233
Thr Ala Lys Glu Val Leu Thr Asp Gly Thr Ser Lys Glu Val Leu Lys
340
gag ata ctt act tgt gat aaa ttt aaa gag gaa gta aca gga gat ggt1281
Glu Ile Leu Thr Cys Asp Lys Phe Lys Glu Ala Val Thr Gly Asp Gly
355
aaa gac ala cta aaa ggt ata ctt aca gut ugc act ggt aag ttt aaal329
Lys Asp Ile Leu Lys Gly Ile Leu Thr Asp Ser Thr Gly Lys Phe Lys
370
gaa ctt atu guu agt act ggt aaa qac ata ctg aaa qac att ctt aca1377
Glu Leu Ile Glu Ser Thr Gly Lys Asp Ile Leu Lys Asp Ile Leu Thr

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          390          395          400
gat aqc act ggt aaa ttt auu gaa ctt ata gaa gta ctg gta aag aac1425
Aap Ser Thr Gly Lys Phe Lys Glu Leu Ile Glu Val Leu Val Lys Asn
          405          410          415
aag cta aaa gag att ctt aca gat uuc acc ggt aac ltc uua ggg ctt1473
Lys Leu Lys Glu Ile Leu Thr Asp Asn Thr Gly Asn Phe Lys Gly Leu
          420          425          430
gta gaa ggc gcc ggg aag gat gaa gca aaa gca gta ctt act gac gag1521
Val Glu Gly Ala Gly Lys Asp Glu Ala Lys Ala Val Leu Thr Asp Glu
          435          440          445
aaa ttt aaa ggc lty ttt gat gac aaa aca ata gct ggc tat gta aau1569
Lys Phe Lys Gly Leu Phe Asp Asp Lys Thr Ile Ala Gly Tyr Val Lys
          450          455          460
gaa ata ctc acc agc gag aag ttt aaa aaa ctg ttt gaa agl gca ggt1617
Glu Ile Leu Thr Ser Glu Lys Phe Lys Leu Phe Glu Ser Ala Gly
          470          475          480
aag act aaa gta aaa gaa ctc ctc att gal gag aag ttt caa aaa ttu1665
Lys Thr Lys Val Lys Glu Leu Leu Ile Asp Glu Lys Phe Gln Lys Leu
          485          490          495
ttt gag gat gac acg aaa gcc agt cal gtu uua gaa ata ctc acg uac1713
Phe Glu Asp Asp Thr Lys Ala Scr His Val Lys Gln Lys Thr Asn
          500          505          510
gut aca gct aag gaa ala ctt uca gat caa aca gct aau gaa gtc cta1761
Asp Thr Ala Lys Glu Ile Leu Thr Asp Gln Thr Ala Lys Glu Val Leu
          515          520          525
aag gat agt acu gct aaa gag ata tta aag gac aca aac gca gct gcg1809
Lys Asp Ser Thr Ala Lys Glu Ile Leu Lys Asp Thr Asn Ala Ala Ala
          530          535          540
cta cta aaa gac agc acu gca aaa gag gta cta aaa tcc gat aaa ttt1857
Leu Leu Lys Asp Scr Thr Ala Lys Glu Val Leu Lys Ser Asp Lys Phe
          550          555          560
aaa gat gca ata act ggt gct ggl aag guc gca cta aaa gag ala ctt1905
Lys Asp Ala Ile Thr Gly Ala Gly Lys Asp Ala Leu Lys Glu Ile Leu
          565          570          575
act tgt gat aau ttt aaa gag gca gta aca ggc aat ggt aau gac ata1953
Thr Cys Asp Lys Phe Lys Glu Ala Val Thr Gly Asn Gly Lys Asp Ile
          580          585          590
cta aau ggt ata ctt aca gat ago act ggt aaa ttt aaa gag cta ata2001
Leu Lys Gly Ile Leu Thr Asp Ser Thr Gly Lys Phe Lys Glu Leu Ile
          595          600          605
gaa agc act ggt aag gat aag cta aau gag att ctt aca gat aac acc2049
Glu Ser Thr Gly Lys Asp Lys Leu Lys Glu Ile Leu Thr Asp Asn Thr
          610          615          620
ggt aac ttt uuu ttt ctt gta gaa gcc gcc ggt aag gat gaa gca aaa2097
Gly Asn Phe Lys Phe Leu Val Glu Gly Ala Gly Lys Asp Glu Ala Lys
          630          635          640
gca gtu ctt act cac gag aaa ttt aaa gac ttg ttt aat gtc aaa aca2145
Ala Val Leu Thr His Glu Lys Phe Lys Asp Leu Phe Asn Val Lys Thr
          645          650          655
aca gct ggc tac gtg aaa gaa ata ctt acc agc gac aag ttt aaa gaa2193
Thr Ala Gly Tyr Val Lys Glu Ile Leu Thr Ser Asp Lys Phe Lys Glu
          660          665          670
ctg ttt act gat gca aca aaa gct gcc tac gtg aua gaa ata ctc acq2241
Leu Phe Thr Asp Ala Thr Lys Ala Gly Tyr Val Lys Glu Ile Leu Thr
          675          680          685
aac gat aca gct aag gaa ata ctt aca gat caa aca gct aaa gaa gtc2289
Asn Asp Thr Ala Lys Glu Ile Leu Thr Asp Gln Thr Ala Lys Glu Val

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690          695          700          705
cta aag gat ggt aca gct aaa gac ata tta aag gac aca aac gca cgt2337
Leu Lys Asp Gly Thr Ala Lys Asp Ile Leu Lys Asp Thr Asn Ala Arg
          710          715          720
gcg cta cta aaa gac agc aca gcc aaa gaa gta cta aaa tgc gat aaa2385
Ala Leu Leu Lys Asp Ser Thr Ala Lys Glu Val Leu Lys Cys Asp Lys
          725          730          735
ttt aag gaa gca ata aca ggt gcc ggl aaa gat gag cta aaa tac ata2433
Phe Lys Glu Ala Ile Thr Gly Ala Gly Lys Asp Glu Leu Lys Tyr Ile
          740          745          750
ctc act aat agc gag ttt aaa agc tta ttt cat agc aad gat agc gct2481
Leu Thr Asn Ser Glu Phe Lys Ser Leu Phe His Ser Lys Asp Ser Ala
          755          760          765
gaa gct gtt aaa gca ala ttt acc cac aat aag ttt aaa gaa cta ctt2529
Glu Ala Val Lys Ala Ile Phe Thr His Asn Lys Phe Lys Glu Leu Leu
          770          775          780          785
gaa cat gca aga aca acc cua aca ata cgc agg cgc ttt gca aat gct2577
Glu His Ala Arg Thr Thr Gln Thr Ile Arg Arg Arg Phe Ala Asn Ala
          790          795          800
tta gat caa cta aaa gcg cta att acc tyt ggc aac ggt gat cat gca2625
Leu Asp Gln Leu Lys Ala Leu Ile Thr Cys Gly Ser Gly Asp His Ala
          805          810          815
aca aaa cta caa gcc ttt gga agt gca cta tgc acc aaa aag aag gag2673
Thr Lys Leu Gln Ala Phe Gly Ser Ala Leu Cys Thr Lys Lys Lys Glu
          820          825          830          835
ttg tgc agt aat ttt agc tgt gca aac tgc agt agt aca act gaa2721
Leu Cys Ser Asn Phe Ser Cys Ala Asn Cys Ser Ser Thr Thr Thr Ala
          840          845
taattacgta gcgctagggtg ggggtaattt acccccacct agctaqaatc acacggggaa 2781
ctttctctctt attactagggt tcttaggatt tacaacacaa ttactatgac agcca 2836

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<200> SEQUENCE CHARACTERISTICS:

<210> SEQ ID NO 4

<211> LENGTH: 849

<212> TYPE: PRT

<213> ORGANISM: *Ehrlichia risticii*

<400> SEQUENCE: 4

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Met Ser Asn Glu Thr Leu Leu Ser Val Leu Ser Asp Glu Thr His Phe
  1          5          10          15
Ala Asn Leu Val Asp Glu Leu Leu Leu Ile Leu Val Lys Asp Ser Ile
  20          25          30
Phe Thr Gln Val Ile Lys Gly Glu Gly Lys Thr Glu Leu Lys Asp Ile
  35          40          45
Leu Thr Asp Asn Thr Gly Lys Phe Lys Glu Leu Ile Gln Ser Ala Gly
  50          55          60
Lys Asp Ile Leu Lys Glu Ile Leu Thr Asp Asn Thr Gly Asn Phe Lys
  65          70          75          80
Gly Leu Ile Glu Gly Asn Gly Lys Thr Glu Ala Lys Glu Val Arg Thr
  85          90          95
Asn Glu Lys Phe Lys Glu Leu Phe Gly Ser Asn Gly Lys Asp Ile Leu
  100          105          110
Lys Asp Ile Leu Thr Asp Asn Thr Gly Asn Phe Lys Gly Leu Ile Glu
  115          120          125
Ser Ala Ala Lys Gly Lys Leu Lys Asp Leu Leu Ile Asp Glu Lys Phe
  130          135          140
Gln Lys Leu Phe Glu Asp Glu Thr Lys Ala Gly Arg Val Lys Glu Ile
  145          150          155          160

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Leu Thr Asp Ser Asn Ala Lys Glu Ile Leu Thr Asn Glu Val Ala Lys
 165 170 175
 Glu Val Leu Lys Ser Asp Lys Phe Lys Glu Ala Ile Thr Gly Asp Gly
 180 185 190
 Lys Asp Ala Leu Lys Glu Ile Leu Thr Cys Asp Lys Phe Lys Glu Ala
 195 200 205
 Val Thr Gly Asn Gly Lys Asp Ile Leu Lys Gly Ile Leu Thr Asp Ser
 210 215 220
 Thr Gly Lys Phe Lys Glu Leu Ile Gln Ser Thr Ser Lys Asp Ile Leu
 225 230 235 240
 Lys Glu Ile Leu Thr Asp Asn Thr Gly Asn Phe Lys Gly Leu Ile Clu
 245 250 255
 Ser Thr Gly Lys Glu Lys Val Lys Glu Leu Leu Ile Asp Gly Lys Phe
 260 265 270
 Lys Asp Leu Phe Thr Asp Ala Thr Lys Ala Gly Tyr Val Lys Glu Ile
 275 280 285
 Leu Thr Asn Asp Thr Ala Lys Glu Val Leu Thr Asp Gln Thr Ala Lys
 290 295 300
 Glu Val Leu Lys Asp Ser Thr Ala Lys Asp Ile Leu Lys Asp Thr Asn
 305 310 315 320
 Ala Ala Ala Val Leu Lys Asn Ser Thr Ala Lys Glu Ile Leu Thr Asn
 325 330 335
 Gln Thr Ala Lys Glu Val Leu Thr Asp Gly Thr Ser Lys Glu Val Leu
 340 345 350
 Lys Glu Ile Leu Thr Cys Asp Lys Phe Lys Glu Ala Val Thr Gly Asp
 355 360 365
 Gly Lys Asp Ile Leu Lys Gly Ile Leu Thr Asp Ser Thr Gly Lys Phe
 370 375 380
 Lys Glu Leu Ile Glu Ser Thr Gly Lys Asp Ile Leu Lys Asp Ile Leu
 385 390 395 400
 Thr Asp Ser Thr Gly Lys Phe Lys Glu Leu Ile Glu Val Leu Val Lys
 405 410 415
 Asn Lys Leu Lys Glu Ile Leu Thr Asp Asn Thr Gly Asn Phe Lys Gly
 420 425 430
 Leu Val Glu Gly Ala Gly Lys Asp Glu Ala Lys Ala Val Leu Thr Asp
 435 440 445
 Glu Lys Phe Lys Gly Leu Phe Asp Asp Lys Thr Ile Ala Gly Tyr Val
 450 455 460
 Lys Glu Ile Leu Thr Ser Glu Lys Phe Lys Lys Leu Phe Glu Ser Ala
 465 470 475 480
 Gly Lys Thr Lys Val Lys Glu Leu Leu Ile Asp Glu Lys Phe Gln Lys
 485 490 495
 Leu Phe Glu Asp Asp Thr Lys Ala Ser His Val Lys Glu Ile Leu Thr
 500 505 510
 Asn Asp Thr Ala Lys Glu Ile Leu Thr Asp Gln Thr Ala Lys Gln Val
 515 520 525
 Leu Lys Asp Ser Thr Ala Lys Glu Ile Leu Lys Asp Thr Asn Ala Ala
 530 535 540
 Ala Leu Leu Lys Asp Ser Thr Ala Lys Glu Val Leu Lys Ser Asp Lys
 545 550 555 560
 Phe Lys Asp Ala Ile Thr Gly Ala Gly Asp Ala Leu Lys Glu Ile
 565 570 575
 Leu Thr Cys Asp Lys Phe Lys Glu Ala Val Thr Gly Asn Gly Lys Asp
 580 585 590
 Ile Leu Lys Gly Ile Leu Thr Asp Ser Thr Gly Lys Phe Lys Glu Leu
 595 600 605
 Ile Glu Ser Thr Gly Lys Asp Lys Leu Lys Glu Ile Leu Thr Asp Asn

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        610                      615                      620
Thr Gly Asn Phe Lys Phe Leu Val Glu Gly Ala Gly Lys Asp Glu Ala
625                      630                      635                      640
Lys Ala Val Leu Thr His Glu Lys Phe Lys Asp Leu Phe Asn Val Lys
        645                      650                      655
Thr Thr Ala Gly Tyr Val Lys Glu Ile Leu Thr Ser Asp Lys Phe Lys
        660                      665                      670
Glu Leu Phe Thr Asp Ala Thr Lys Ala Gly Tyr Val Lys Glu Ile Leu
        675                      680                      685
Thr Asn Asp Thr Ala Lys Glu Ile Leu Thr Asp Gln Thr Ala Lys Glu
690                      695                      700
Val Leu Lys Asp Gly Thr Ala Lys Asp Ile Leu Lys Asp Thr Asn Ala
705                      710                      715                      720
Arg Ala Leu Leu Lys Asp Ser Thr Ala Lys Glu Val Leu Lys Cys Asp
        725                      730                      735
Lys Phe Lys Glu Ala Ile Thr Gly Ala Gly Lys Asp Glu Leu Lys Tyr
        740                      745                      750
Ile Leu Thr Asn Ser Glu Phe Lys Ser Leu Phe His Ser Lys Asp Ser
        755                      760                      765
Ala Glu Ala Val Lys Ala Ile Phe Thr His Asn Lys Phe Lys Glu Leu
770                      775                      780
Leu Glu His Ala Arg Thr Thr Gln Thr Ile Arg Arg Arg Phe Ala Asn
785                      790                      795                      800
Ala Leu Asp Gln Leu Lys Ala Leu Ile Thr Cys Gly Ser Gly Asp His
        805                      810                      815
Ala Thr Lys Leu Gln Ala Phe Gly Ser Ala Leu Cys Thr Lys Lys Lys
        820                      825                      830
Glu Leu Cys Ser Asn Phe Ser Cys Ala Asn Cys Ser Ser Thr Thr Thr
        835                      840                      845
Ala

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<200> SEQUENCE CHARACTERISTICS:

<210> SEQ ID NO 5

<211> LENGTH: 1937

<212> TYPE: DNA

<213> ORGANISM: Ehrlichia risticii

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1/5)..(1791)

<400> SEQUENCE: 5

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ttaaatttta tgattttttta taataaaaat agatataaaa lltagttautt ttataaattt 120
tttataacua aggactaccc tcctacata aaatttctau gucgaaaaat ccct atg 177

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Met

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tcu aat gaa aca ctt ctg ago gla ctt tct gat gaa acg cac ttt gcl225
Ser Asn Glu Thr Leu Leu Ser Val Leu Ser Asp Glu Thr His Phe Ala
        5                      10                      15
aat cta gtt gat gaa ctt ctt ctc agc ttg gtt aaa gac agt att ttc273
Asn Leu Val Asp Glu Leu Leu Leu Ser Leu Val Lys Asp Ser Ile Phe
        20                      25                      30
act caa gta ata aaa ggc gag gga aag ucu gaa tta aaa gac att ctt321
Thr Gln Val Ile Lys Gly Glu Gly Lys Thr Glu Leu Lys Asp Ile Leu
        35                      40                      45
aca gat agc act ggc aag ttt aaa gag ctg ata gga agt agc ggt aag369
Thr Asp Ser Thr Gly Lys Phe Lys Glu Leu Ile Gly Ser Ser Gly Lys
        50                      55                      60                      65

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gat atu cta aaa agc ata cac aca gat ggc tca ggc aac ttt aaa ggc417
Asp Ile Leu Lys Ser Ile His Thr Asp Gly Ser Gly Asn Phe Lys Gly
70 75 80
ctt ata caa agc aca ggt aag gca gaa gta aaa gag gta ctc act aat465
Leu Ile Gln Ser Thr Gly Lys Ala Glu Val Lys Glu Val Leu Thr Asn
85 90 95
gaa aaa ttc aaa gag ctt ttt gga agc gaa ggt aaa gac ata cta aaa513
Glu Lys Phe Lys Glu Leu Phe Gly Ser Glu Gly Lys Asp Ile Leu Lys
100 105 110
gag ata ctt oca gac aat acc ggc aut ttt aaa ggt ctt ala gaa ggc561
Glu Ile Leu Thr Asp Asn Thr Gly Asn Phe Lys Gly Leu Ile Glu Gly
115 120 125
aaa ggt aag gal gaa gca aag gga gta ctt act gac gag aaa ttt aaa609
Lys Gly Lys Asp Glu Ala Lys Gly Val Leu Thr Asp Glu Lys Phe Lys
130 135 140 145
ggc ttg ttt gat gac aaa acu ata gct ggc tat gta aaa gaa ata ctc657
Gly Leu Phe Asp Asp Lys Thr Ile Ala Gly Tyr Val Lys Glu Ile Leu
150 155 160
acc agc gag agt tta auu uac tgt ttg aaa ggt gca ggt aag act aaa705
Thr Ser Glu Ser Leu Lys Asn Cys Leu Lys Gly Ala Gly Lys Thr Lys
165 170 175
gta uaa gaa ctc ctc att gat gag aag ttt caa aaa tta ttt gag gat753
Val Lys Glu Leu Leu Ile Asp Glu Lys Phe Gln Lys Leu Phe Glu Asp
180 185 190
gac acg aaa gcc agl cat gta uaa gaa ata ctt aca gac agt aac gct801
Asp Thr Lys Ala Ser His Val Lys Glu Ile Leu Thr Asp Ser Asn Ala
195 200 205
aag gaa ata ctc aca aat gaa gta gca aaa gag gta cta aaa tcc gat849
Lys Glu Ile Leu Thr Asn Glu Val Ala Lys Glu Val Leu Lys Ser Asp
210 215 220 225
aaa ttt aaa gal gca ata act ggt gct ggt aag gac gca cta aaa gag897
Lys Phe Lys Asp Ala Ile Thr Gly Ala Gly Lys Asp Ala Leu Lys Glu
230 235 240
ata ctt act tgc gat aaa ttt aaa gat gca gta aca ggt aat ggt aag945
Ile Leu Thr Cys Asp Lys Phe Lys Asp Ala Val Thr Gly Asn Gly Lys
245 250 255
gac gca cta auu gaa ata ctt act tgc gat aaa ttt aaa gat gca gta993
Asp Ala Leu Lys Glu Ile Leu Thr Cys Asp Lys Phe Lys Asp Ala Val
260 265 270
acu ggc aat ggt aaa gac aag cta aaa gag all ctt act cuc gag aag1041
Thr Gly Asn Gly Lys Asp Lys Leu Lys Glu Ile Thr His Glu Lys
275 280 285
ttt aaa gca ctc ala gag agt gaa ggc aaa gac ata ctc aca gaa att1089
Phe Lys Ala Leu Ile Glu Ser Glu Gly Lys Asp Ile Leu Lys Glu Ile
290 295 300 305
ctt aca gat agt acc ggt aaa ttt aaa gag cta ata gaa agc act ggt1137
Leu Thr Asp Ser Thr Gly Lys Phe Lys Glu Leu Ile Glu Ser Thr Gly
310 315 320
aaa gac aag cta aaa gag att ttc aca gal aac acc ggt aac ttt aaal185
Lys Asp Lys Leu Lys Glu Ile Phe Thr Asp Asn Thr Gly Asn Phe Lys
325 330 335
ggg ctt gta gaa ggc gcc ggt aag gat gaa gca aaa gca gta ctt act1233
Gly Leu Val Glu Gly Ala Gly Lys Asp Glu Ala Lys Ala Val Leu Thr
340 345 350
cac gag aaa ttt aaa gac ttg ttt aat gac aaa aca aca gcl ggc tac1281
His Glu Lys Phe Lys Asp Leu Phe Asn Asp Lys Thr Thr Ala Gly Tyr
355 360 365

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gtg aaa gaa ata ctc acc agt gat aag ttt aaa aaa tta ttt gag gac1329
Val Lys Glu Ile Leu Thr Ser Asp Lys Phe Lys Lys Leu Phe Glu Asp
370                               375                               380                               385
aat acc aaa gct qgc tac gtg aaa gaa ala ctc ugc aac gat aca gct1377
Asn Thr Lys Ala Gly Tyr Val Lys Glu Ile Leu Thr Asn Asp Thr Ala
390                               395                               400
aag gaa atu ctc aca aat caa aca gct aaa gaa gtc cta aaa gac agc1425
Lys Glu Ile Leu Thr Asn Gln Thr Ala Lys Glu Val Leu Lys Asp Ser
405                               410                               415
aca gcc aaa gaa ata cta aaa tgc gat aaa ttt aag gac gca ata aca1473
Thr Ala Lys Glu Ile Leu Lys Cys Asp Lys Phe Lys Asp Ala Ile Thr
420                               425                               430
ggc gct ggt aaa gat gaq cta aaa tac ata ctc act aat aac gag ttt1521
Gly Ala Gly Lys Asp Glu Leu Lys Tyr Ile Leu Thr Asn Asn Glu Phe
435                               440                               445
aaa agc tta ttt gat agc aag gat ugc gct gaa gct gtt aaa gca atu1569
Lys Ser Leu Phe Asp Ser Lys Asp Ser Ala Glu Ala Val Lys Ala Ile
450                               455                               460
ttt acc cac aat aag ttt aaa gaa cta ctt aaa acg lyc aag gac aac1617
Phe Thr His Asn Lys Phe Lys Glu Leu Leu Lys Thr Cys Lys Asp Asn
470                               475                               480
cca aaa aat acg gcg gcg ctt gca gct gct tta gat gaa cta aaa gal1665
Pro Lys Asn Thr Ala Ala Leu Ala Ala Ala Leu Asp Glu Leu Lys Asp
485                               490                               495
cta att acg tgt gac cgc aat aat cat gca aca aaa cta caa gcc ttt1713
Leu Ile Thr Cys Asp Arg Asn Asn His Ala Thr Lys Leu Gln Ala Phe
500                               505                               510
gga agt gca cta tgc acc aga aau uuu gag tcg tgc gat aat ttt agc1761
Gly Ser Ala Leu Cys Thr Arg Lys Lys Glu Ser Cys Asp Asn Phe Ser
515                               520                               525
cct gca agc tgc agt agt aca gca gct aca taattacgta gcgctaggtg 1811
Pro Ala Ser Cys Ser Ser Thr Ala Ala Thr
530                               535
ggggtaaat accccacac acgtagaatc acacggggaa cttctctctc attactgagg 1871
tcttaggatt taactllcaaa ttactatgac agccgattaa attatkatga cagacgatac 1931
actttt 1937

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<200> SEQUENCE CHARACTERISTICS:

<210> SEQ ID NO 6

<211> LENGTH: 539

<212> TYPE: PRT

<213> ORGANISM: Ehrlichia risticii

<400> SEQUENCE: 6

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Ala Asn Leu Val Asp Glu Leu Leu Leu Ser Leu Val Lys Asp Ser Ile
20                               25                               30
Phe Thr Gln Val Ile Lys Gly Glu Gly Lys Thr Glu Leu Lys Asp Ile
35                               40                               45
Leu Thr Asp Ser Thr Gly Lys Phe Lys Glu Leu Ile Gly Ser Ser Gly
50                               55                               60
Lys Asp Ile Leu Lys Ser Ile His Thr Asp Gly Ser Gly Asn Phe Lys
65                               70                               75                               80
Gly Leu Ile Gln Ser Thr Gly Lys Ala Glu Val Lys Glu Val Leu Thr
85                               90                               95
Asn Glu Lys Phe Lys Glu Leu Phe Gly Ser Glu Gly Lys Asp Ile Leu
100                               105                               110

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Lys Glu Ile Leu Thr Asp Asn Thr Gly Asn Phe Lys Gly Leu Ile Glu
 115 120 125
 Gly Lys Gly Lys Asp Glu Ala Lys Gly Val Leu Thr Asp Glu Lys Phe
 130 135 140
 Lys Gly Leu Phe Asp Asp Lys Thr Ile Ala Gly Tyr Val Lys Glu Ile
 145 150 155 160
 Leu Thr Ser Glu Ser Leu Lys Asn Cys Leu Lys Gly Ala Gly Lys Thr
 165 170 175
 Lys Val Lys Glu Leu Leu Ile Asp Glu Lys Phe Gln Lys Leu Phe Glu
 180 185 190
 Asp Asp Thr Lys Ala Ser His Val Lys Glu Ile Leu Thr Asp Ser Asn
 195 200 205
 Ala Lys Glu Ile Leu Thr Asn Glu Val Ala Lys Glu Val Leu Lys Ser
 210 215 220
 Asp Lys Phe Lys Asp Ala Ile Thr Gly Ala Gly Lys Asp Ala Leu Lys
 225 230 235 240
 Glu Ile Leu Thr Cys Asp Lys Phe Lys Asp Ala Val Thr Gly Asn Gly
 245 250 255
 Lys Asp Ala Leu Lys Glu Ile Leu Thr Cys Asp Lys Phe Lys Asp Ala
 260 265 270
 Val Thr Gly Asn Gly Lys Asp Lys Leu Lys Glu Ile Leu Thr His Glu
 275 280 285
 Lys Phe Lys Ala Leu Ile Glu Ser Glu Gly Lys Asp Ile Leu Lys Glu
 290 295 300
 Ile Leu Thr Asp Ser Thr Gly Lys Phe Lys Glu Leu Ile Glu Ser Thr
 305 310 315 320
 Gly Lys Asp Lys Leu Lys Glu Ile Phe Thr Asp Asn Thr Gly Asn Phe
 325 330 335
 Lys Gly Leu Val Glu Gly Ala Gly Lys Asp Glu Ala Lys Ala Val Leu
 340 345 350
 Thr His Glu Lys Phe Lys Asp Leu Phe Asn Asp Lys Thr Thr Ala Gly
 355 360 365
 Tyr Val Lys Glu Ile Leu Thr Ser Asp Lys Phe Lys Lys Leu Phe Glu
 370 375 380
 Asp Asn Thr Lys Ala Gly Tyr Val Lys Glu Ile Leu Thr Asn Asp Thr
 385 390 395 400
 Ala Lys Glu Ile Leu Thr Asn Gln Thr Ala Lys Glu Val Leu Lys Asp
 405 410 415
 Ser Thr Ala Lys Glu Ile Leu Lys Cys Asp Lys Phe Lys Asp Ala Ile
 420 425 430
 Thr Gly Ala Gly Lys Asp Glu Leu Lys Tyr Ile Leu Thr Asn Asn Glu
 435 440 445
 Phe Lys Ser Leu Phe Asp Ser Lys Asp Ser Ala Glu Ala Val Lys Ala
 450 455 460
 Ile Phe Thr His Asn Lys Phe Lys Glu Leu Leu Lys Thr Cys Lys Asp
 465 470 475 480
 Asn Pro Lys Asn Thr Ala Ala Leu Ala Ala Leu Asp Glu Leu Lys
 485 490 495
 Asp Leu Ile Thr Cys Asp Arg Asn Asn His Ala Thr Lys Leu Gln Ala
 500 505 510
 Phe Gly Ser Ala Leu Cys Thr Arg Lys Lys Glu Ser Cys Asp Asn Phe
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 Ser Pro Ala Ser Cys Ser Ser Thr Ala Ala Thr
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<210> SEQ ID NO 7

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<212> TYPE: DNA
<213> ORGANISM: Ehrlichia risticii
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ttcataacaa aggactalcc tccctgcata aaatttctaa gacgaaaaat cttt atg 177
Met
1
tca aat gaa aca ctt ctg agc gta ctt lct gut gaa acg cnc ttt gct 225
Ser Asn Glu Thr Leu Leu Ser Val Leu Ser Asp Glu Thr His Phe Ala
5 10 15
aat cta gtt gat gaa ctt ctt ctg agc agt att ttc 273
Asn Leu Val Asp Glu Leu Leu Ser Leu Val Lys Asp Ser Ile Phe
20 25 30
act caa gta ata aaU ggc gag gga aag aca gaa lta aaU gac att ctt 321
Thr Gln Val Ile Lys Gly Glu Gly Lys Thr Glu Leu Lys Asp Ile Leu
35 40 45
aca gat agc act ggc aug ttt aaa gag ctg ata gga agt agc ggt aag 369
Thr Asp Ser Thr Gly Lys Phe Lys Glu Leu Ile Gly Ser Ser Gly Lys
50 55 60
gat ata ctu aaa agc ata ctg aca gat ggc tca ggc uac ttt aaa ggc 417
Asp Ile Leu Lys Ser Ile Leu Thr Asp Gly Ser Gly Asn Phe Lys Gly
65 70 75
ctt ata caa agc aca ggt aag gca gaa gta aaa gag gta ctg act aal 465
Leu Ile Gln Ser Thr Gly Lys Ala Glu Val Lys Glu Val Leu Thr Asn
80 85 90 95
gaa aaU ttc aaa gag ctt ttt gga agc gal ggt aag gut ata tta aaa 513
Glu Lys Phe Lys Glu Leu Phe Gly Ser Asp Gly Lys Asp Ile Leu Lys
100 105 110
gac ata ctg aca gal agc act ggt aug ttt aaa gag ctg ata gga agl 561
Asp Ile Leu Thr Asp Ser Thr Gly Lys Phe Lys Glu Leu Ile Gly Ser
115 120 125
agc ggt aag gac ata cta aaa aac att ctt uca gat agc acc ggt aag 609
Ser Gly Lys Asp Ile Leu Lys Asn Ile Leu Thr Asp Ser Thr Gly Lys
130 135 140 145
ttt aaa gaa ctt ata gaa agl gca ggt aag ggt aag ctg aaa gac ctt 657
Phe Lys Glu Leu Ile Glu Ser Ala Gly Lys Gly Lys Leu Lys Asp Leu
150 155 160
ctt att gat gga aac ttt aaa aaa tta ttt gag gal gac agc aaa gct 705
Leu Ile Asp Gly Asn Phe Lys Lys Leu Phe Glu Asp Asp Thr Lys Ala
165 170 175
gct cat gta aaU gaa ata cll aca gac agc uac gct aag gaa ata ctg 753
Ala His Val Lys Glu Ile Leu Thr Asp Ser Asn Ala Lys Glu Ile Leu
180 185 190
aca aat gaa gta gca aaa gag gta cta aaU tcc gat aaa ttt aaa gat 801
Thr Asn Glu Val Ala Lys Glu Val Leu Lys Ser Asp Lys Phe Lys Asp
195 200 205
gca ata act ggt gct ggt aag gac gca cta aaa gag ata cll act tgc 849
Ala Ile Thr Gly Ala Gly Lys Asp Ala Leu Lys Glu Ile Leu Thr Cys
210 215 220 225
gat aaa ttt aaa gal gca gta aca ggc aat ggt aag gac gca cta aaa 897
Asp Lys Phe Lys Asp Ala Val Thr Gly Asn Gly Lys Asp Ala Leu Lys
230 235 240

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gaa ata ctt acL tgc gat aaa ttt aaa gat gca gta uca ggc aat ggt 945
Glu Ile Leu Thr Cys Asp Lys Phe Lys Asp Ala Val Thr Gly Asn Gly
245 250 255
aaa gac aaq cta aaa gag att ctt acL cac gag aag ttt aaa gca ctc 993
Lys Asp Lys Leu Lys Glu Ile Leu Thr His Glu Lys Phe Lys Ala Leu
260 265 270
ata gag agt gaa ggc aaa gac ala ctg aaa gac att ctt aca gat 1041
Ile Glu Ser Glu Gly Lys Asp Ile Leu Lys Asp Ile Leu Thr Asp Ser
275 280 285
acc ggt aaa ttt aaq gag cta ata gaa aqc acg ggt aag gat gaa gca 1089
Thr Gly Lys Phe Lys Glu Leu Ile Glu Ser Thr Gly Lys Asp Glu Ala
290 295 300
aaa gca gta ctt act gac gag aaa ttt auu qac ttg ttt aat gac aaal137
Lys Ala Val Leu Thr Asp Glu Lys Phe Lys Asp Leu Phe Asn Asp Lys
310 315 320
aca aca gct ggc tac gtg aaa gaa ala ctc acc agt gat aag ttt aaal185
Thr Thr Ala Gly Tyr Val Lys Glu Ile Leu Thr Ser Asp Lys Phe Lys
325 330 335
aaa tta ttt gag gac aat acc aaa gct ggc tac gtg aaa gaa ata ctc 1233
Lys Leu Phe Glu Asp Asn Thr Lys Ala Gly Tyr Val Lys Glu Ile Leu
340 345 350
acg aac gat aca gct aag gaa ata ctt acc aat cat aaa ttt aag gaal281
Thr Asn Asp Thr Ala Lys Glu Ile Leu Thr Asn His Lys Phe Lys Glu
355 360 365
gca ata act ggc gat ggt aaa gac ata ctg aaa guu att ctt aca gat 1329
Ala Ile Thr Gly Asp Gly Lys Asp Ile Leu Lys Glu Ile Leu Thr Asp
370 375 380
agc act ggt aac ttt aaa ggc gca ata aca ggt gcc ggt aaa gat cag 1377
Ser Thr Gly Asn Phe Lys Gly Ala Ile Thr Gly Ala Gly Lys Asp Glu
390 395 400
cta aaa tac ata ctc act aat aqc gag ttt aaa agc tta ttt gat agn 1425
Leu Lys Tyr Ile Leu Thr Asn Ser Glu Phe Lys Ser Leu Phe Asp Ser
405 410 415
aaa gat agc gct gaa gct gtt aaa gaa ata ttt acc cac agl aag ttt 1473
Lys Asp Ser Ala Glu Ala Val Lys Glu Ile Phe Thr His Ser Lys Phe
420 425 430
aaa gaa cta ctt aaa aag tgc aag gac uac cca aaa aat acg gcg gcg 1521
Lys Glu Leu Leu Lys Thr Cys Lys Asp Asn Pro Lys Asn Thr Ala Ala
435 440 445
ctt gca gct gct tta gat gaa cta aaa gat cta att acc lgt ggc ugc 1569
Leu Ala Ala Ala Leu Asp Glu Leu Lys Asp Leu Ile Thr Cys Gly Ser
450 455 460
ggt gat cat gca aca aaa cta caa gcc lll gga agt gca cta tgc acc 1617
Gly Asp His Ala Thr Lys Leu Glu Ala Phe Gly Ser Ala Leu Cys Thr
470 475 480
aga aaa aaa gag tgc tgc gat aal llt aqc tct gca uac tgc agt agt 1665
Arg Lys Lys Glu Ser Cys Asp Asn Phe Ser Ser Ala Asn Cys Ser Ser
485 490 495
aca aca act gca taattacgta qcgctaggcg ggggtaattt accccacct 1717
Thr Thr Thr Ala
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<200> SEQUENCE CHARACTERISTICS:

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<211> LENGTH: 501

<212> TYPE: PRT

<213> ORGANISM: Ehrlichia risticii

<400> SEQUENCE: 8

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 1           5           10           15
Ala Asn Leu Val Asp Glu Leu Leu Ser Leu Val Lys Asp Ser Ile
 20           25           30
Phe Thr Gln Val Ile Lys Gly Glu Gly Lys Thr Glu Leu Lys Asp Ile
 35           40           45
Leu Thr Asp Ser Thr Gly Lys Phe Lys Glu Leu Ile Gly Ser Ser Gly
 50           55           60
Lys Asp Ile Leu Lys Ser Ile Leu Thr Asp Gly Ser Gly Asn Phe Lys
 65           70           75
Gly Leu Ile Gln Ser Thr Gly Lys Ala Glu Val Lys Glu Val Leu Thr
 85           90           95
Asn Glu Lys Phe Lys Glu Leu Phe Gly Ser Asp Gly Lys Asp Ile Leu
100           105           110
Lys Asp Ile Leu Thr Asp Ser Thr Gly Lys Phe Lys Glu Leu Ile Gly
115           120           125
Ser Ser Gly Lys Asp Ile Leu Lys Asn Ile Leu Thr Asp Ser Thr Gly
130           135           140
Lys Phe Lys Glu Leu Ile Glu Ser Ala Gly Lys Gly Lys Leu Lys Asp
145           150           155           160
Leu Leu Ile Asp Gly Asn Phe Lys Lys Leu Phe Glu Asp Asp Thr Lys
165           170           175
Ala Ala His Val Lys Glu Ile Leu Thr Asp Ser Asn Ala Lys Glu Ile
180           185           190
Leu Thr Asn Glu Val Ala Lys Glu Val Leu Lys Ser Asp Lys Phe Lys
195           200           205
Asp Ala Ile Thr Gly Ala Gly Lys Asp Ala Leu Lys Glu Ile Leu Thr
210           215           220
Cys Asp Lys Phe Lys Asp Ala Val Thr Gly Asn Gly Lys Asp Ala Leu
225           230           235           240
Lys Glu Ile Leu Thr Cys Asp Lys Phe Lys Asp Ala Val Thr Gly Asn
245           250           255
Gly Lys Asp Lys Leu Lys Glu Ile Leu Thr His Glu Lys Phe Lys Ala
260           265           270
Leu Ile Glu Ser Glu Gly Lys Asp Ile Leu Lys Asp Ile Leu Thr Asp
275           280           285
Ser Thr Gly Lys Phe Lys Glu Leu Ile Glu Ser Thr Gly Lys Asp Glu
290           295           300
Ala Lys Ala Val Leu Thr Asp Glu Lys Phe Lys Asp Leu Phe Asn Asp
305           310           315           320
Lys Thr Thr Ala Gly Tyr Val Lys Glu Ile Leu Thr Ser Asp Lys Phe
325           330           335
Lys Lys Leu Phe Glu Asp Asn Thr Lys Ala Gly Tyr Val Lys Glu Ile
340           345           350
Leu Thr Asn Asp Thr Ala Lys Glu Ile Leu Thr Asn His Lys Phe Lys
355           360           365
Glu Ala Ile Thr Gly Asp Gly Lys Asp Ile Leu Lys Glu Ile Leu Thr
370           375           380
Asp Ser Thr Gly Asn Phe Lys Gly Ala Ile Thr Gly Ala Gly Lys Asp
385           390           395           400
Gln Leu Lys Tyr Ile Leu Thr Asn Ser Glu Phe Lys Ser Leu Phe Asp
405           410           415
Ser Lys Asp Ser Ala Glu Ala Val Lys Glu Ile Phe Thr His Ser Lys
420           425           430

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Phe Lys Glu Leu Leu Lys Thr Cys Lys Asp Asn Pro Lys Asn Thr Ala
    435          440          445
Ala Leu Ala Ala Ala Leu Asp Glu Leu Lys Asp Leu Ile Thr Cys Gly
    450          455          460
Ser Gly Asp His Ala Thr Lys Leu Gln Ala Phe Gly Ser Ala Leu Cys
    465          470          475          480
Thr Arg Lys Lys Glu Ser Cys Asp Asn Phe Ser Ser Ala Asn Cys Ser
    485          490          495
Ser Thr Thr Thr Ala
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<210> SEQ ID NO 9

<211> LENGTH: 33

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence primer

<400> SEQUENCE: 9

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33

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<210> SEQ ID NO 10

<211> LENGTH: 33

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence primer

<400> SEQUENCE: 10

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33

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<210> SEQ ID NO 11

<211> LENGTH: 18

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

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<400> SEQUENCE: 11

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18

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<211> LENGTH: 18

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence primer

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18

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<211> LENGTH: 18

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence primer
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<220> FEATURE:
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<211> LENGTH: 11
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<200> SEQUENCE CHARACTERISTICS:
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<212> TYPE: DNA
<213> ORGANISM: Ehrlichia risticii
<400> SEQUENCE: 18
gaaatactca c 11

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aaagacutac t 11

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<213> ORGANISM: Ehrlichia risticii
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<400> SEQUENCE: 23
attttttata a 11

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<213> ORGANISM: Ehrlichia risticii
<400> SEQUENCE: 24
aaactttaag g 11

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<211> LENGTH: 11
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<213> ORGANISM: Ehrlichia risticii
<400> SEQUENCE: 25
aagtttaag a 11

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<211> LENGTH: 11
<212> TYPE: DNA
<213> ORGANISM: Ehrlichia risticii
<400> SEQUENCE: 26
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<200> SEQUENCE CHARACTERISTICS:
<210> SEQ ID NO 27
<211> LENGTH: 11
<212> TYPE: DNA
<213> ORGANISM: Ehrlichia risticii
<400> SEQUENCE: 27
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11

<200> SEQUENCE CHARACTERISTICS:
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<212> TYPE: DNA
<213> ORGANISM: Ehrlichia risticii
<400> SEQUENCE: 28
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11

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11

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11

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<212> TYPE: DNA
<213> ORGANISM: Ehrlichia risticii
<400> SEQUENCE: 32
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11

<200> SEQUENCE CHARACTERISTICS:
<210> SEQ ID NO 33
<211> LENGTH: 11
<212> TYPE: DNA
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11

<200> SEQUENCE CHARACTERISTICS:

<210> SEQ ID NO 34
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<400> SEQUENCE: 34
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11

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<212> TYPE: DNA
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11

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<210> SEQ ID NO 36
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<212> TYPE: DNA
<213> ORGANISM: Ehrlichia risticii
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11

<200> SEQUENCE CHARACTERISTICS:
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gaaataactta c

11

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<211> LENGTH: 11
<212> TYPE: DNA
<213> ORGANISM: Ehrlichia risticii
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11

<200> SEQUENCE CHARACTERISTICS:
<210> SEQ ID NO 39
<211> LENGTH: 11
<212> TYPE: DNA
<213> ORGANISM: Ehrlichia risticii
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gataaattta a

11

<200> SEQUENCE CHARACTERISTICS:
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<213> ORGANISM: Ehrlichia risticii
<400> SEQUENCE: 40
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11

<200> SEQUENCE CHARACTERISTICS:
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<211> LENGTH: 11
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<213> ORGANISM: Ehrlichia risticii
<400> SEQUENCE: 41
gaaataactca c 11

<200> SEQUENCE CHARACTERISTICS:
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<211> LENGTH: 11
<212> TYPE: DNA
<213> ORGANISM: Ehrlichia risticii
<400> SEQUENCE: 42
accggtaact t 11

<200> SEQUENCE CHARACTERISTICS:
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<211> LENGTH: 11
<212> TYPE: DNA
<213> ORGANISM: Ehrlichia risticii
<400> SEQUENCE: 43
atgcaacaaa a 11

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<211> LENGTH: 11
<212> TYPE: DNA
<213> ORGANISM: Ehrlichia risticii
<400> SEQUENCE: 44
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<200> SEQUENCE CHARACTERISTICS:
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<211> LENGTH: 11
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<400> SEQUENCE: 45
cttacaguta a 11

<200> SEQUENCE CHARACTERISTICS:
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<211> LENGTH: 11
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<213> ORGANISM: Ehrlichia risticii
<400> SEQUENCE: 46
gcaataactg g 11

<200> SEQUENCE CHARACTERISTICS:
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<211> LENGTH: 11
<212> TYPE: DNA
<213> ORGANISM: Ehrlichia risticii
<400> SEQUENCE: 47
atggtaagga c 11

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<211> LENGTH: 11

<212> TYPE: DNA
<213> ORGANISM: Ehrlichia risticii
<400> SEQUENCE: 18
acttatagaa g

11

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